FIG. 1

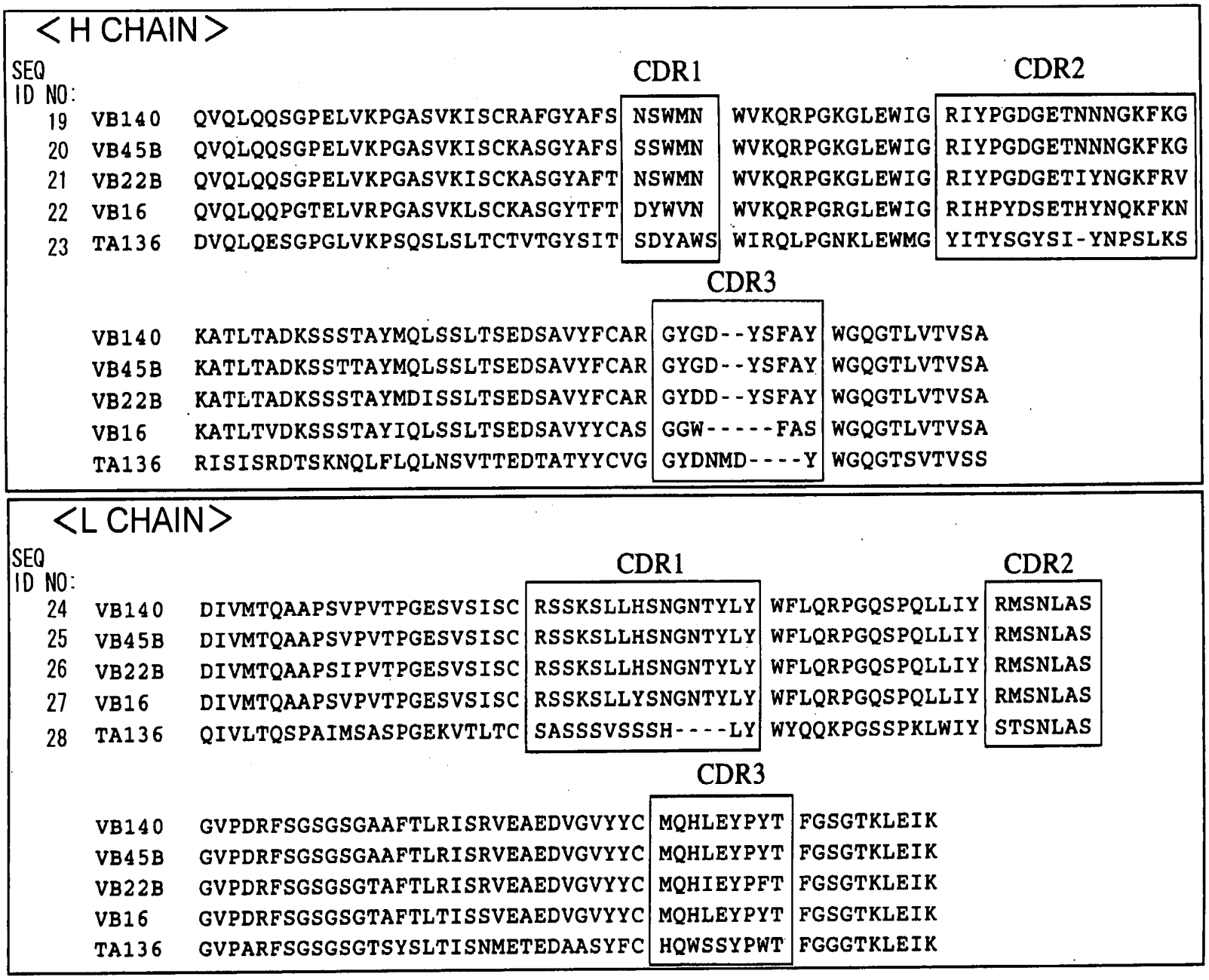

<H CHAIN>
SEQ ID NO:
CDR1
CDR2
19 VB140 QVQLQQSGPELVKPGASVKISCRAFGYAFS NSWMN WVKQRPGKGLEWIG RIYPGDGETNNNGKFKG
20 VB45B QVQLQQSGPELVKPGASVKISCKASGYAFS SSWMN WVKQRPGKGLEWIG RIYPGDGETNNNGKFKG
21 VB22B QVQLQQSGPELVKPGASVKISCKASGYAFT NSWMN WVKQRPGKGLEWIG RIYPGDGETIYNGKFRV
22 VB16 QVQLQQPGTELVRPGASVKLSCKASGYTFT DYWVN WVKQRPGRGLEWIG RIHPYDSETHYNQKFKN
23 TA136 DVQLQESGPGLVKPSQSLSLTCTVTGYSIT SDYAWS WIRQLPGNKLEWMG YITYSGYSI-YNPSLKS
CDR3
VB140 KATLTADKSSSTAYMQLSSLTSEDSAVYFCAR GYGD--YSFAY WGQGTLVTVSA
VB45B KATLTADKSSTTAYMQLSSLTSEDSAVYFCAR GYGD--YSFAY WGQGTLVTVSA
VB22B KATLTADKSSSTAYMDISSLTSEDSAVYFCAR GYDD--YSFAY WGQGTLVTVSA
VB16 KATLTVDKSSSTAYIQLSSLTSEDSAVYYCAS GGW-----FAS WGQGTLVTVSA
TA136 RISISRDTSKNQLFLQLNSVTTEDTATYYCVG GYDNMD----Y WGQGTSVTVSS
<L CHAIN>
SEQ ID NO:
CDR1
CDR2
24 VB140 DIVMTQAAPSVPVTPGESVSISC RSSKSLLHSNGNTYLY WFLQRPGQSPQLLIY RMSNLAS
25 VB45B DIVMTQAAPSVPVTPGESVSISC RSSKSLLHSNGNTYLY WFLQRPGQSPQLLIY RMSNLAS
26 VB22B DIVMTQAAPSIPVTPGESVSISC RSSKSLLHSNGNTYLY WFLQRPGQSPQLLIY RMSNLAS
27 VB16 DIVMTQAAPSVPVTPGESVSISC RSSKSLLYSNGNTYLY WFLQRPGQSPQLLIY RMSNLAS
28 TA136 QIVLTQSPAIMSASPGEKVTLTC SASSSVSSSH----LY WYQQKPGSSPKLWIY STSNLAS
CDR3
VB140 GVPDRFSGSGSGAAFTLRISRVEAEDVGVYYC MQHLEYPYT FGSGTKLEIK
VB45B GVPDRFSGSGSGAAFTLRISRVEAEDVGVYYC MQHLEYPYT FGSGTKLEIK
VB22B GVPDRFSGSGSGTAFTLRISRVEAEDVGVYYC MQHIEYPFT FGSGTKLEIK
VB16 GVPDRFSGSGSGTAFTLTISSVEAEDVGVYYC MQHLEYPYT FGSGTKLEIK
TA136 GVPARFSGSGSGTSYSLTISNMETEDAASYFC HQWSSYPWT FGGGTKLEIK

FIG. 2

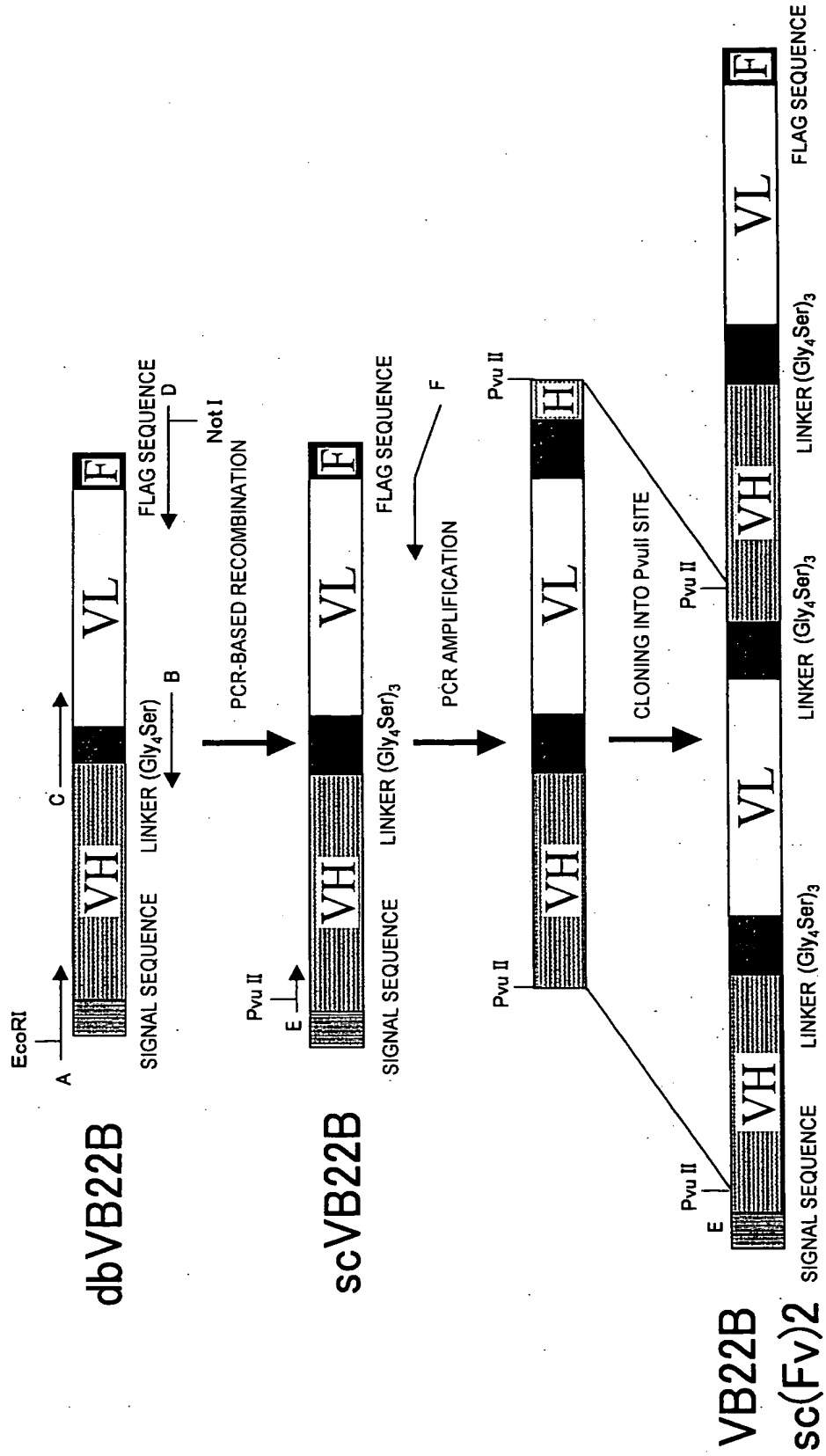

dbVB22B
EcoRI
A
SIGNAL SEQUENCE
VH
C
LINKER (Gly4Ser)
B
VL
FLAG SEQUENCE
D
F
Not I
PCR-BASED RECOMBINATION
scVB22B
Pvu II
E
SIGNAL SEQUENCE
VH
LINKER (Gly4Ser)3
VL
FLAG SEQUENCE
F
PCR AMPLIFICATION
Pvu II
VH
VL
CLONING INTO PvuII SITE
VB22B
sc(Fv)2
Pvu II
E
SIGNAL SEQUENCE
VH
LINKER (Gly4Ser)3
VL
Pvu II
LINKER (Gly4Ser)3
VH
VL
FLAG SEQUENCE
F

FIG. 3

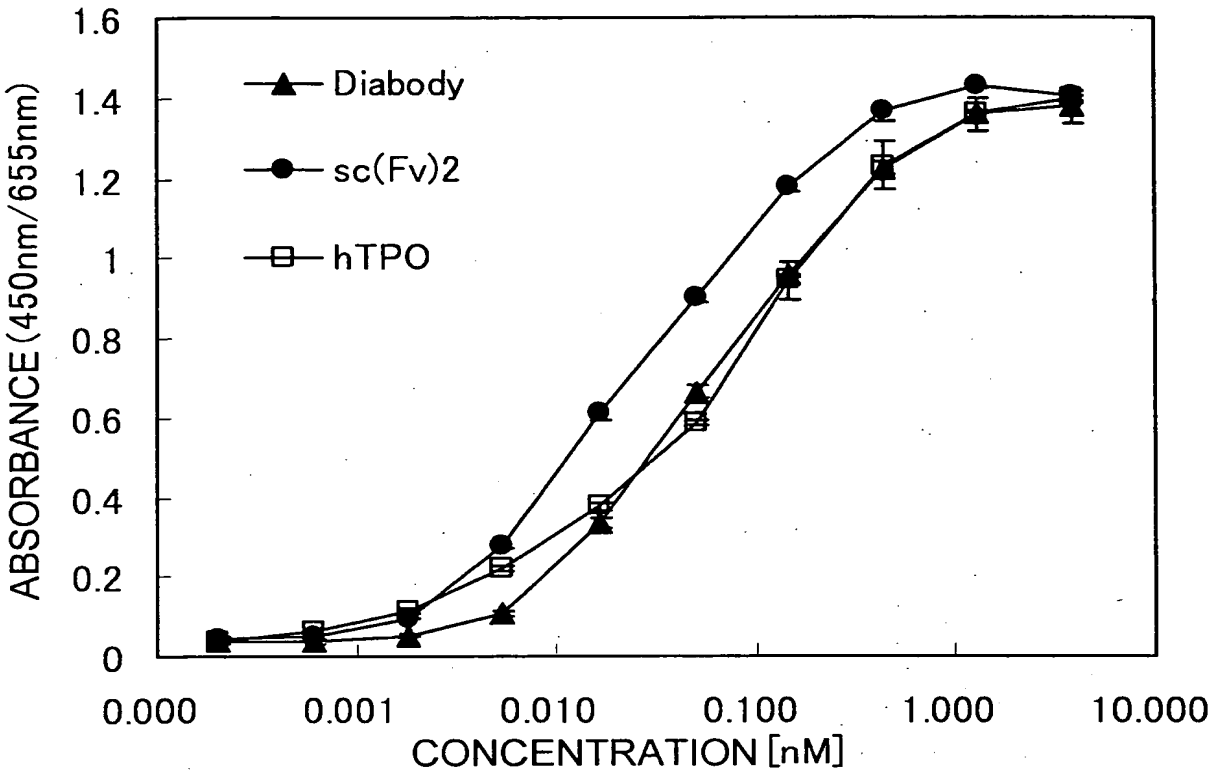

1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
ABSORBANCE (450nm/655nm)
Diabody
sc(Fv)2
hTPO
0.000
0.001
0.010
0.100
1.000
10.000
CONCENTRATION [nM]

FIG. 4

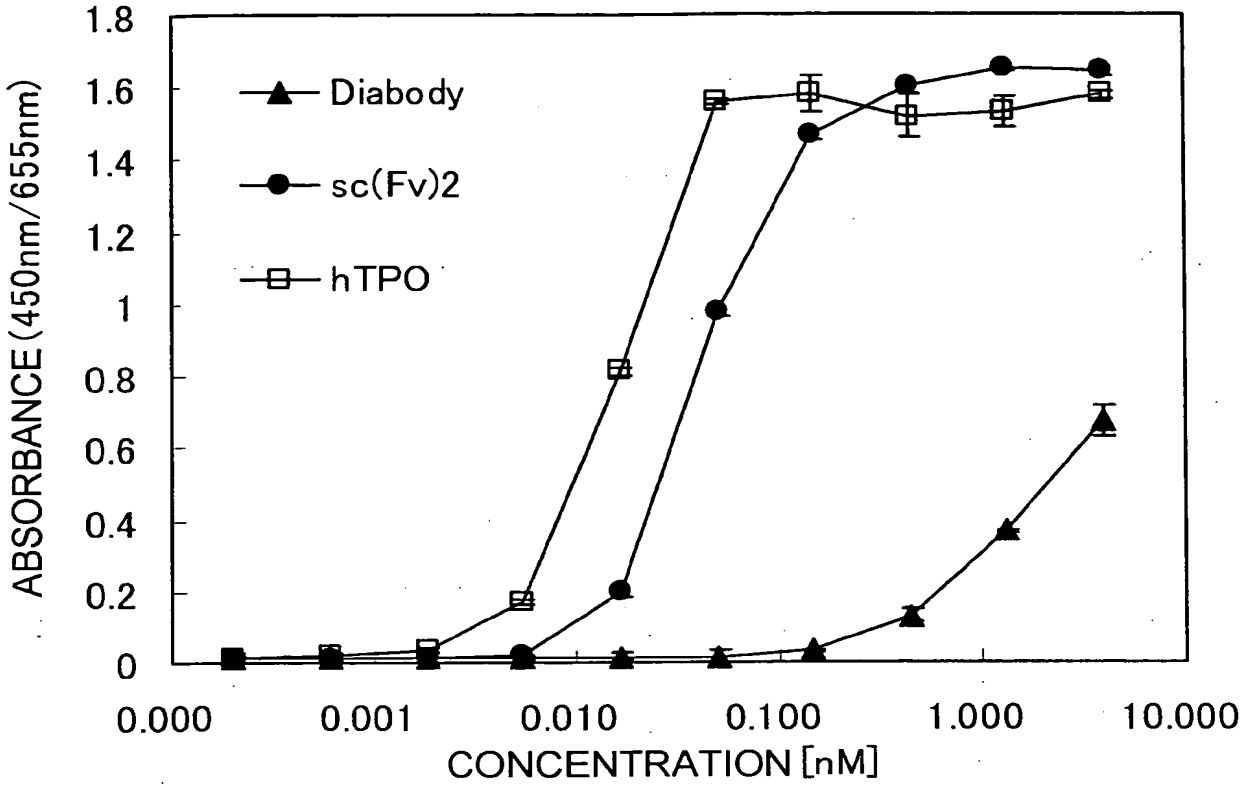

1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
ABSORBANCE(450nm/655nm)
Diabody
sc(Fv)2
hTPO
0.000
0.001
0.010
0.100
1.000
10.000
CONCENTRATION [nM]

FIG. 5

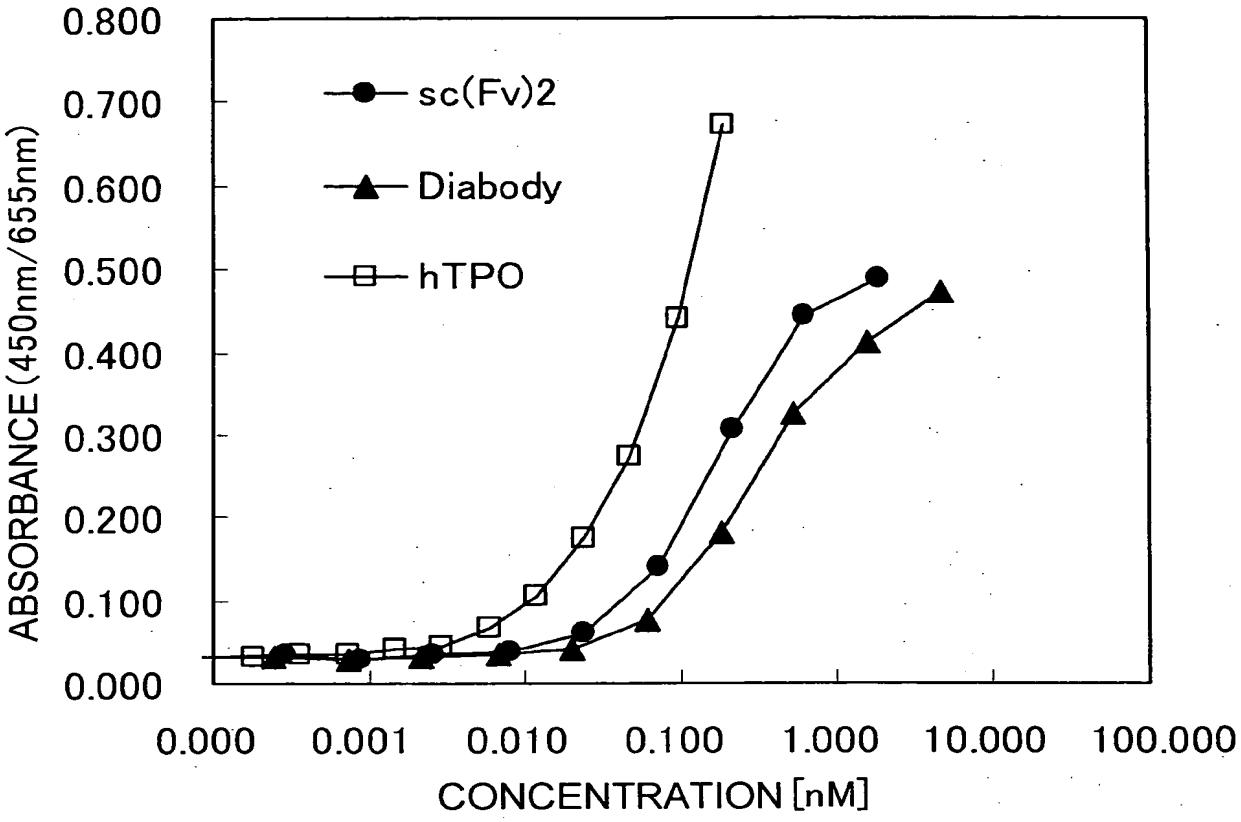

0.800
0.700
0.600
0.500
0.400
0.300
0.200
0.100
0.000
ABSORBANCE (450nm/655nm)
sc(Fv)2
Diabody
hTPO
0.000
0.001
0.010
0.100
1.000
10.000
100.000
CONCENTRATION [nM]

FIG. 6

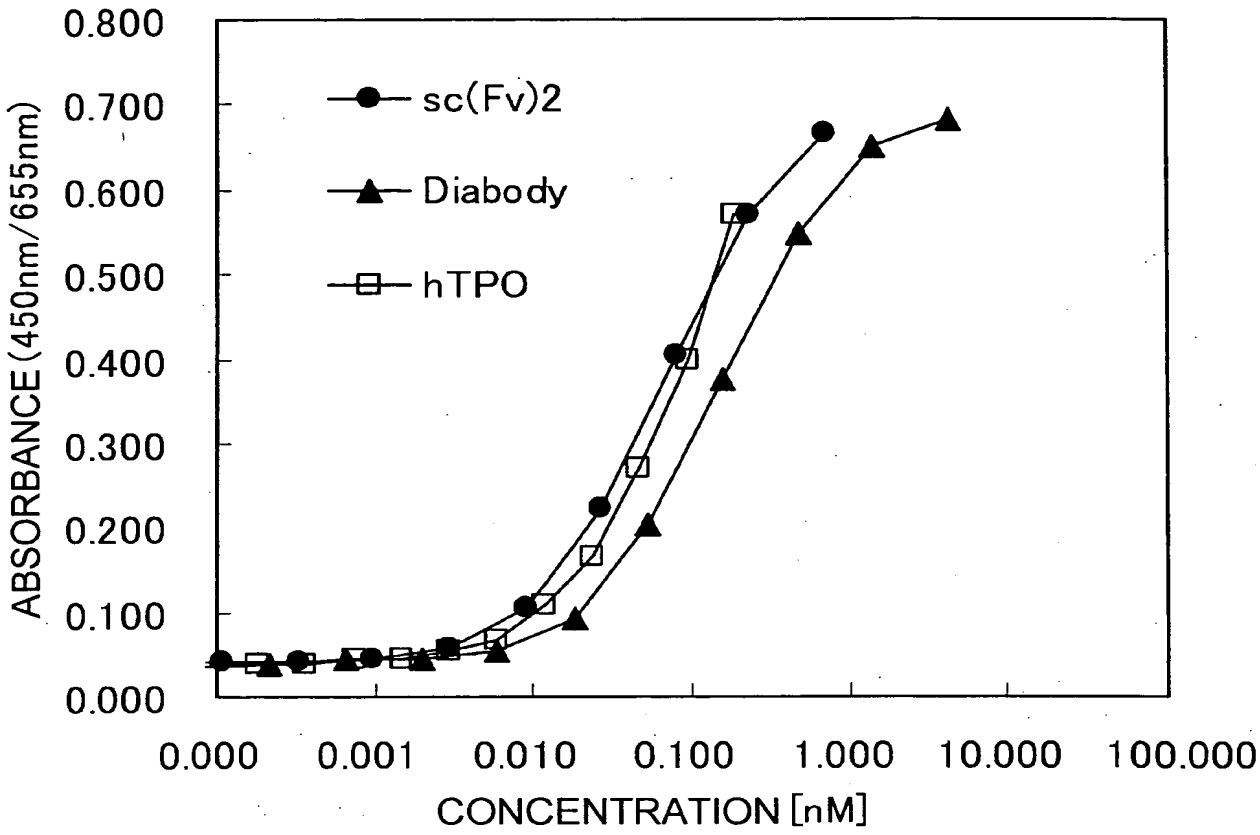

0.800
0.700
0.600
0.500
0.400
0.300
0.200
0.100
0.000
ABSORBANCE (450nm/655nm)
sc(Fv)2
Diabody
hTPO
0.000
0.001
0.010
0.100
1.000
10.000
100.000
CONCENTRATION [nM]

FIG. 7

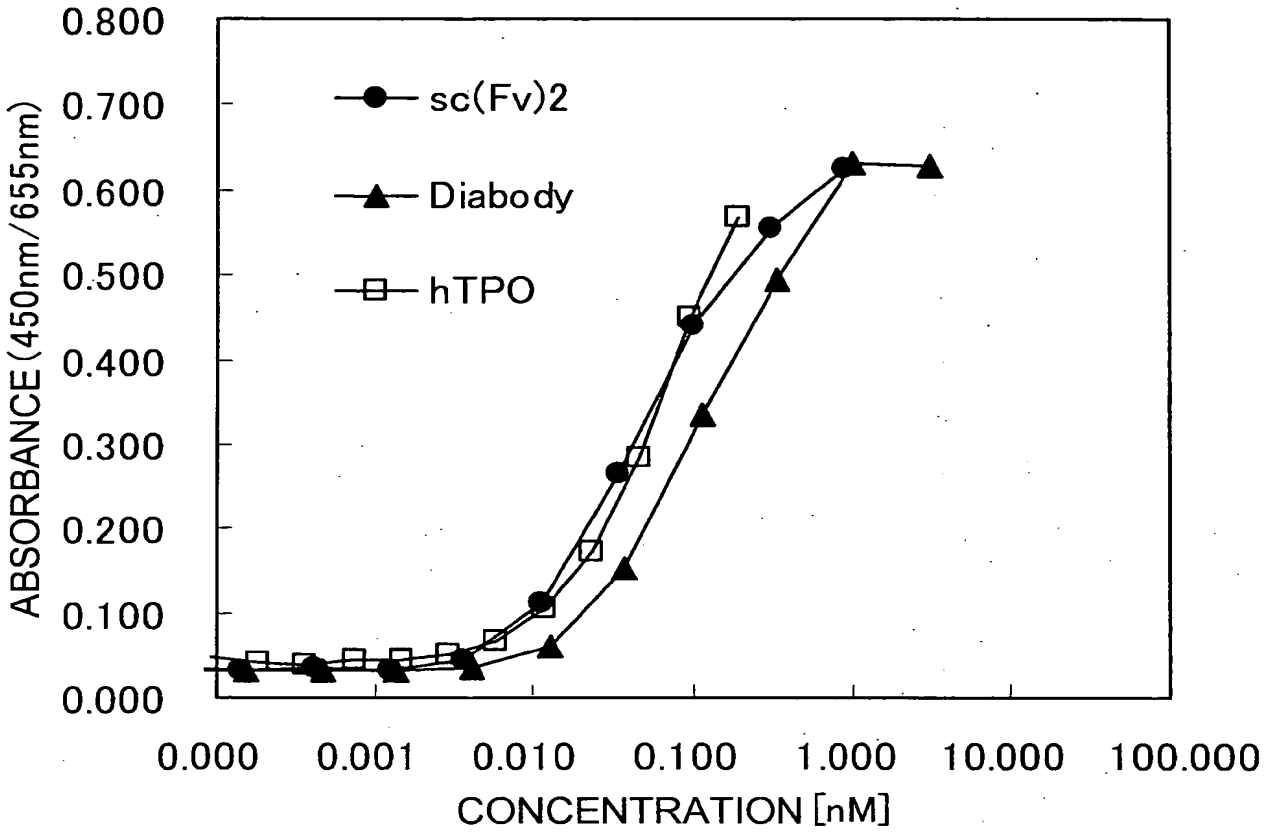
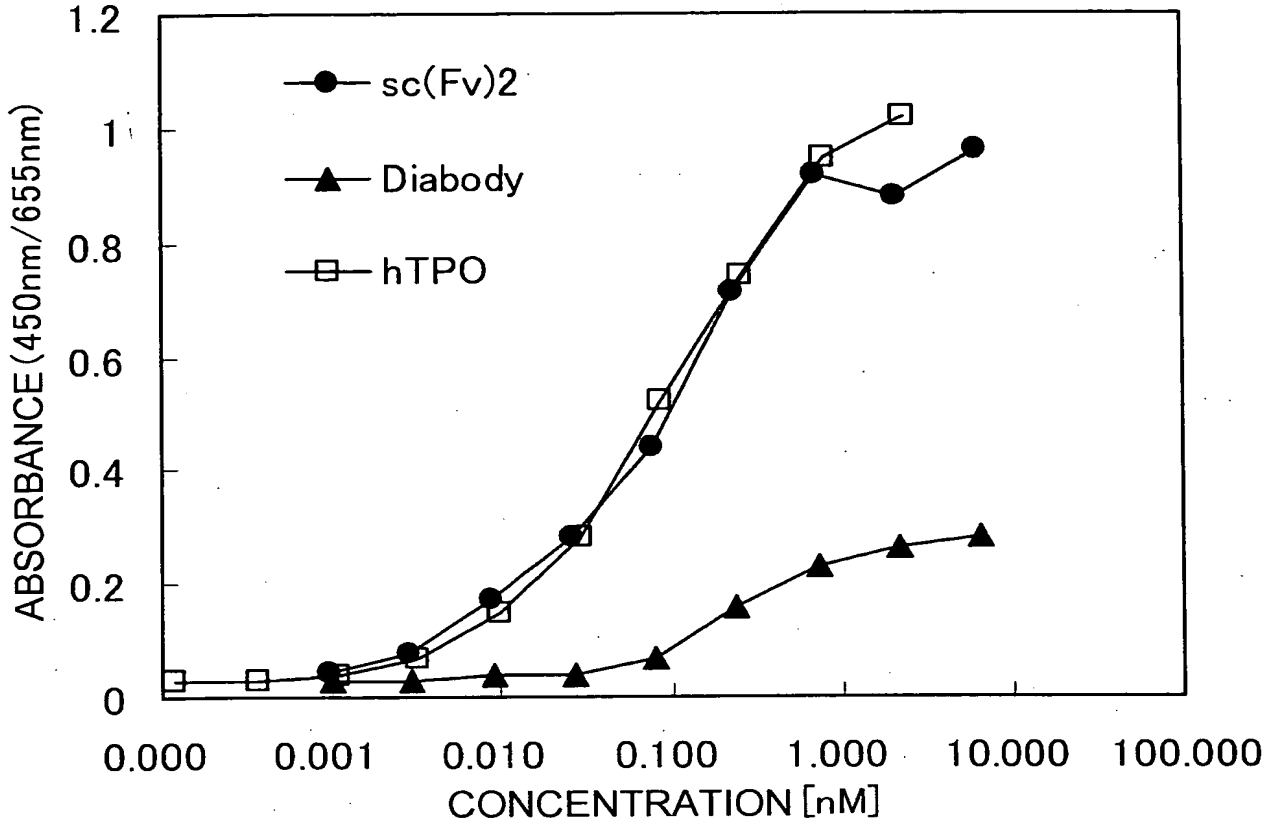

0.800
0.700
0.600
0.500
0.400
0.300
0.200
0.100
0.000
ABSORBANCE (450nm/655nm)
sc(Fv)2
Diabody
hTPO
0.000
0.001
0.010
0.100
1.000
10.000
100.000
CONCENTRATION [nM]

FIG. 8


1.2
1
0.8
0.6
0.4
0.2
0
ABSORBANCE (450nm/655nm)
sc(Fv)2
Diabody
hTPO
0.000
0.001
0.010
0.100
1.000
10.000
100.000
CONCENTRATION [nM]